

SEQUENCE LISTING

<110> Fuso Pharmaceutical Industries Ltd.

<120> Novel serine protease BSSP5

5 <130> 661640

<150> JP 10-347806

<151> 1998-11-20

<160> 32

10 <210> 1

<211> 1149

<212> DNA

<213> human

15 <400> 1

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-30

-25

-20

20 tgg ggc tgc ggc att cct gcc atc aaa ccg gca ctg agc ttc agc cag agg 109

Trp Gly Cys Gly Ile Pro Ala Ile Lys Pro Ala Leu Ser Phe Ser Gln Arg

-15

-10

-5

-1

att gtc aac ggg gag aat gca gtg ttg ggc tcc tgg ccc tgg cag gtg tcc 160

Ile Val Asn Gly Glu Asn Ala Val Leu Gly Ser Trp Pro Trp Gln Val Ser

25

1

5

10

15

P01250-070095860

ctg cag gac agc ggc ttc cac ttc tgc ggt ggt tct ctc atc agc cag 211
 Leu Gln Asp Ser Ser Gly Phe His Phe Cys Gly Gly Ser Leu Ile Ser Gln
 20 25 30
 tcc tgg gtg gtc act gct gcc cac tgc aat gtc agc cct ggc cgc cat ttt 262
 5 Ser Trp Val Val Thr Ala Ala His Cys Asn Val Ser Pro Gly Arg His Phe
 35 40 45 50
 gtt gtc ctg ggc gag tat gac cga tca tca aac gca gag ccc ttg cag gtt 313
 Val Val Leu Gly Glu Tyr Asp Arg Ser Ser Asn Ala Glu Pro Leu Gln Val
 55 60 65
 10 ctg tcc gtc tct cgg gcc att aca cac cct agc tgg aac tct acc acc atg 364
 Leu Ser Val Ser Arg Ala Ile Thr His Pro Ser Trp Asn Ser Thr Thr Met
 70 75 80 85
 aac aat gac gtg acg ctg ctg aag ctc gcc tcg cca gcc cag tac aca aca 415
 Asn Asn Asp Val Thr Leu Leu Lys Leu Ala Ser Pro Ala Gln Tyr Thr Thr
 15 90 95 100
 cgc atc tcg cca gtt tgc ctg gca tcc tca aac gag gct ctg act gaa ggc 466
 Arg Ile Ser Pro Val Cys Leu Ala Ser Ser Asn Glu Ala Leu Thr Glu Gly
 105 110 115
 ctc acg tgt gtc acc acc ggc tgg ggt cgc ctc agt ggc gtg ggc aat gtg 517
 20 Leu Thr Cys Val Thr Thr Gly Trp Gly Arg Leu Ser Gly Val Gly Asn Val
 120 125 130 135
 aca cca gca cat ctg cag cag gtg gct ttg ccc ctg gtc act gtg aat cag 568
 Thr Pro Ala His Leu Gln Gln Val Ala Leu Pro Leu Val Thr Val Asn Gln
 140 145 150
 25 tgc cgg cag tac tgg gac tca agt atc act gac tcc atg atc tgt gca ggt 619

Cys Arg Gln Tyr Trp Asp Ser Ser Ile Thr Asp Ser Met Ile Cys Ala Gly
 155 160 165 170
 ggc gca ggt gcc tcc tcg tgc cag ggt gac tcc gga ggc cct ctt gtc tgc 670
 Gly Ala Gly Ala Ser Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys
 5 175 180 185
 cag aag gga aac aca tgg gtg ctt att ggt att gtc tcc tgg ggc acc aaa 721
 Gln Lys Gly Asn Thr Trp Val Leu Ile Gly Ile Val Ser Trp Gly Thr Lys
 190 195 200
 aac tgc aat gtg cgc gca cct gct gtg tat act cga gtt agc aag ttc agc 772
 10 Asn Cys Asn Val Arg Ala Pro Ala Val Tyr Thr Arg Val Ser Lys Phe Ser
 205 210 215 220
 acc tgg atc aac cag gtc ata gcc tac aac tga gctcaccaca ggccctcccc 825
 Thr Trp Ile Asn Gln Val Ile Ala Tyr Asn
 225 230
 15 agctcaaccc atttaaagga cccaggccct gtcccatcat gcattcatgt ctgtttccct 885
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 aaggggctga gtgactcctt gagtagcagt ggctttccct agagtagcca tgccgtggcc 1005
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 20 ttacaaaaaa aaaaaaaaaa aaaa 1149

<210> 2
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 <212> PRT
 25 <213> human

<400> 2

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5 Trp Gly Cys Gly Ile Pro Ala Ile Lys Pro Ala Leu Ser Phe Ser Gln Arg

-15 -10 -5 -1

Ile Val Asn Gly Glu Asn Ala Val Leu Gly Ser Trp Pro Trp Gln Val Ser

1 5 10 15

Leu Gln Asp Ser Ser Gly Phe His Phe Cys Gly Gly Ser Leu Ile Ser Gln

10 20 25 30

Ser Trp Val Val Thr Ala Ala His Cys Asn Val Ser Pro Gly Arg His Phe

35 40 45 50

Val Val Leu Gly Glu Tyr Asp Arg Ser Ser Asn Ala Glu Pro Leu Gln Val

55 60 65

15 Leu Ser Val Ser Arg Ala Ile Thr His Pro Ser Trp Asn Ser Thr Thr Met

70 75 80 85

Asn Asn Asp Val Thr Leu Leu Lys Leu Ala Ser Pro Ala Gln Tyr Thr Thr

90 95 100

Arg Ile Ser Pro Val Cys Leu Ala Ser Ser Asn Glu Ala Leu Thr Glu Gly

20 105 110 115

Leu Thr Cys Val Thr Thr Gly Trp Gly Arg Leu Ser Gly Val Gly Asn Val

120 125 130 135

Thr Pro Ala His Leu Gln Gln Val Ala Leu Pro Leu Val Thr Val Asn Gln

140 145 150

25 Cys Arg Gln Tyr Trp Asp Ser Ser Ile Thr Asp Ser Met Ile Cys Ala Gly

DRAFT 5.0 1995-05-01

155 160 165 170
 Gly Ala Gly Ala Ser Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys
 175 180 185
 Gln Lys Gly Asn Thr Trp Val Leu Ile Gly Ile Val Ser Trp Gly Thr Lys
 5 190 195 200
 Asn Cys Asn Val Arg Ala Pro Ala Val Tyr Thr Arg Val Ser Lys Phe Ser
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 Thr Trp Ile Asn Gln Val Ile Ala Tyr Asn
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 <213> mouse
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 Ser Leu Val Leu Leu Gly Ser Ser Trp Gly Cys Gly Val Pro Ala Ile Thr
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 Pro Ala Leu Ser Tyr Asn Gln Arg Ile Val Asn Gly Glu Asn Ala Val Pro
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1012450 " 6745360

ggc tcc tgg ccc tgg cag gtg tct ctc cag gat aac acc ggc ttc cac ttc 209

Gly Ser Trp Pro Trp Gln Val Ser Leu Gln Asp Asn Thr Gly Phe His Phe

10 15 20 25

tgc ggt ggt tct ctc atc agt ccg aac tgg gtg gtc acg gct gcc cac tgc 260

5 Cys Gly Gly Ser Leu Ile Ser Pro Asn Trp Val Val Thr Ala Ala His Cys

30 35 40

caa gtc acg cct gga cgc cac ttt gtc gtt ttg gga gaa tat gac cga tct 311

Gln Val Thr Pro Gly Arg His Phe Val Val Leu Gly Glu Tyr Asp Arg Ser

45 50 55 60

10 tcc aat gct gaa cct gtg cag gtc ctc tcg atc gca agg gcc atc aca cac 362

Ser Asn Ala Glu Pro Val Gln Val Leu Ser Ile Ala Arg Ala Ile Thr His

65 70 75

cct aac tgg aac gcc aac acc atg aac aat gac ctg act ctc ctg aag ctt 413

Pro Asn Trp Asn Ala Asn Thr Met Asn Asn Asp Leu Thr Leu Lys Leu

15 80 85 90

gcc tcg cca gcc cgg tac aca gca caa gtc tca cca gtc tgc ctg gct tcc 464

Ala Ser Pro Ala Arg Tyr Thr Ala Gln Val Ser Pro Val Cys Leu Ala Ser

95 100 105 110

aca aac gag gca ctg cct tcg ggg ctc acc tgt gtc acc act ggc tgg ggc 515

20 Thr Asn Glu Ala Leu Pro Ser Gly Leu Thr Cys Val Thr Thr Gly Trp Gly

115 120 125

cga atc agt ggt gtg ggc aat gtg aca cca gct cgc ctg cag caa gtt gtt 566

Arg Ile Ser Gly Val Gly Asn Val Thr Pro Ala Arg Leu Gln Gln Val Val

130 135 140 145

25 cta ccc ctg gtc act gtg aat cag tgt cgg cag tac tgg ggt gca cgc att 617

Leu Pro Leu Val Thr Val Asn Gln Cys Arg Gln Tyr Trp Gly Ala Arg Ile
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 acc gat gcc atg ata tgt gca ggt ggc tca ggc gcc tcc tca tgt cag ggt 668
 Thr Asp Ala Met Ile Cys Ala Gly Gly Ser Gly Ala Ser Ser Cys Gln Gly
 5 165 170 175
 gac tca gga ggc cct ctt gtc tgc cag aag gga aac acc tgg gtg ctt att 719
 Asp Ser Gly Gly Pro Leu Val Cys Gln Lys Gly Asn Thr Trp Val Leu Ile
 180 185 190 195
 ggg att gtc tcc tgg ggc act aag aac tgc aac ata caa gca ccg gcc atg 770
 10 Gly Ile Val Ser Trp Gly Thr Lys Asn Cys Asn Ile Gln Ala Pro Ala Met
 200 205 210
 tac act cgg gtc agc aag ttc agt acc tgg atc aac caa gtc atg gcc tac 821
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 215 220 225 230
 15 aac taaactgtcc 834
 Asn

<210> 4
 <211> 264
 20 <212> PRT
 <213> mouse

<400> 4

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 -5 -1 1 5
 5 Gly Ser Trp Pro Trp Gln Val Ser Leu Gln Asp Asn Thr Gly Phe His Phe
 10 15 20 25
 Cys Gly Gly Ser Leu Ile Ser Pro Asn Trp Val Val Thr Ala Ala His Cys
 30 35 40
 Gln Val Thr Pro Gly Arg His Phe Val Val Leu Gly Glu Tyr Asp Arg Ser
 10 45 50 55 60
 Ser Asn Ala Glu Pro Val Gln Val Leu Ser Ile Ala Arg Ala Ile Thr His
 65 70 75
 Pro Asn Trp Asn Ala Asn Thr Met Asn Asn Asp Leu Thr Leu Leu Lys Leu
 80 85 90
 15 Ala Ser Pro Ala Arg Tyr Thr Ala Gln Val Ser Pro Val Cys Leu Ala Ser
 95 100 105 110
 Thr Asn Glu Ala Leu Pro Ser Gly Leu Thr Cys Val Thr Thr Gly Trp Gly
 115 120 125
 Arg Ile Ser Gly Val Gly Asn Val Thr Pro Ala Arg Leu Gln Gln Val Val
 20 130 135 140 145
 Leu Pro Leu Val Thr Val Asn Gln Cys Arg Gln Tyr Trp Gly Ala Arg Ile
 150 155 160
 Thr Asp Ala Met Ile Cys Ala Gly Gly Ser Gly Ala Ser Ser Cys Gln Gly
 165 170 175
 25 Asp Ser Gly Gly Pro Leu Val Cys Gln Lys Gly Asn Thr Trp Val Leu Ile

058350 102509 092509

180 185 190 195

Gly Ile Val Ser Trp Gly Thr Lys Asn Cys Asn Ile Gln Ala Pro Ala Met

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Tyr Thr Arg Val Ser Lys Phe Ser Thr Trp Ile Asn Gln Val Met Ala Tyr

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Asn

<210> 5

<211> 99

10 <212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide to construct plasmid pSecTrypHis

15 <400> 5

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tttgacgacg atgacaagga tccgaattc 99

<210> 6

20 <211> 99

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide to construct plasmid pSecTrypHis

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gaattcggat ccttgtcatc gtcgtcaaag gggcagcaa cagcagcagc aacaaaggta 60 aggatcagga
gttagattcat ggtgttgcta gccaaagctt 99

10 <210> 7

<211> 15

<212> DNA

<213> Artificial Sequence

<220>

15 <223> Designed oligonucleotide primer to amplify neurosin-encoding sequence

20 <400> 7

ttggtgcatg gcgga 15

25 <210> 8

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

30 <223> Designed oligonucleotide primer to amplify neurosin-encoding sequence

35 <400> 8

tcctcgagac ttggcctgaa tggttt 27

40 <210> 9

211 35

<212> DNA

<213> Artificial Sequence

<220>

5 <223> Designed oligonucleotide primer to amplify a portion of plasmid
pSecTrypHis/Neurosin

<400> 9

gcgctagcag atctccatga atctactcct gatcc

35

10

〈210〉 10

29

<212> DNA

<213> Artificial Sequence

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pSecTrypHis/Neurosin

<400> 10

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tgaagcttgc catggaccaa cttgtcatc

29

〈210〉 11

<211> 26

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<213> Artificial Sequence

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<223> Designed oligonucleotide primer to amplify a portion of plasmid pTrypHis

<400> 11

5 ccaagcttca ccatcaccat caccat 26

<210> 12

<211> 17

<212> DNA

10 <213> Artificial Sequence

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<223> Designed oligonucleotide primer to amplify a portion of plasmid
pTrypSigTag

15 <400> 12

gcacagtcga ggctgat 17

<210> 13

<211> 17

20 <212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer to amplify a portion of plasmid
pFBTrypSigTag

400 13

caaatgtggt atggctg

17

210 14

5 211 20

212 DNA

213 Artificial Sequence

220

223 Designed oligonucleotide primer to amplify conserved region of serin
10 proteases-encoding sequence

220

221 UNSURE

220 9, 12

223 n is a, c, g or t.

15

400 14

gtgctcaacng cngcbcaytg

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210 15

20 211 20

212 DNA

213 Artificial Sequence

220

223 Designed oligonucleotide primer to amplify conserved region of serin
25 proteases-encoding sequence

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<221> UNSURE

<220> 12, 15

<223> n is a, c, g or t.

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<400> 15

ccvctrwsdc cnccnggcga

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<210> 16

10 <211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer for RACE for hBSSP5 (forward)

15

<400> 16

tgtcagccct ggccgccatt

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<210> 17

20 <211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer for RACE for hBSSP5 (forward)

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<400> 17

gcgagtatga ccgatcatca

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<210> 18

5 <211> 20

<212> DNA

<213> Artificial Sequence

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<223> Designed oligonucleotide primer for RACE for hBSSP5 (reverse)

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<400> 18

cgccacctgc acagatcatg

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<210> 19

15 <211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer for RACE for hBSSP5 (reverse)

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<400> 19

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length hBSSP5 (forward)

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E02150 "6TE95860

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<210> 24

<211> 20

20 <212> DNA

<213> Artificial Sequence

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<223> Designed oligonucleotide primer designated as mBSSP5F1 for RACE for mBSSP5 (forward)

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210> 25

5 <211> 17

<212> DNA

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10 <223> Designed oligonucleotide primer designated as mBSSP5F2 for RACE for mBSSP5
(forward)

400> 25

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17

15 <210> 26

<211> 20

<212> DNA

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<220>

20 <223> Designed oligonucleotide primer designated as mBSSP5F3 to amplify full
length mBSSP5 (forward)

400> 26

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<210> 27

<211> 20

<212> DNA

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<223> Designed oligonucleotide primer designated as mBSSP5Fmature to amplify
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<210> 28

<211> 20

<212> DNA

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<223> Designed oligonucleotide primer designated as mBSSP5.1 for RACE for mBSSP5
(reverse)

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25 <212> DNA

<213> Artificial Sequence

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(reverse)

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<210> 30

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<212> DNA

<213> Artificial Sequence

220

<223> Designed oligonucleotide primer designated as mBSSP5R3/E to amplify full length mBSSP5 (reverse)

15 length mBSSP5 (reverse)

<400> 30

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27

20 <210> 31

〈211〉 117

<212> DNA

<213> Artificial Sequence

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25 <223> Designed oligonucleotide to construct plasmid pTrypHis

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tgctgcccccc tttcaccatc accatcacca tgacgacgat gacaaggatc cgaattc 117

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〈210〉 32

〈211〉 117

<212> DNA

<213> Artificial Sequence

10 <220>

<223> Designed oligonucleotide to construct plasmid pTrypHis

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gcagcagcaa caaaggtaag gatcaggagt agattcatgg tggcgtagc caagctt 117

15 gcagcagcaa caaaggtaag gatcaggagt agattcatgg tggcttagc caagctt 117

gcagcagcaa caaaggtaag gatcaggagt agattcatgg tggcttagc caagctt 117